

## **REMARKS**

Reconsideration and withdrawal of the rejections set forth in the Office Action dated January 29, 2008 are respectfully requested.

### **I. Amendment to the Abstract**

The Abstract is amended as to correct grammatical errors.

### **II. Amendments to the Claims**

Independent claim 15 is amended to refer to "modules," which represent "a subsequence of the splice variant selected from an exon and an intron." Support for the amendment can be found, *e.g.*, at ¶ [0037].

Claim 15 is further amended to require "applying a second, different, mathematical function to the length of a second subsequence" and that "the scaled length of the first subsequence and the scaled length of the second subsequence are displayed simultaneously." Support for these amendments can be found, *e.g.*, at ¶¶ [0050] and [0084].

Other amendments are made to claim 15 to add clarity.

Claims 16-21 are amended to conform to amended claim 15.

No new matter has been added by these amendments

### **III. Objection to the Abstract**

The Abstract was objected to for containing a grammatical error.

The Abstract has been amended as suggested by the Examiner.

The Abstract has also been amended to improve the grammar of the first sentence.

No new matter has been added by the amendments.

### **IV. Rejections Under 35 U.S.C. § 112, Second Paragraph (Indefiniteness)**

Claims 15-21 were rejected under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite with respect to the language "modules and exons."

Claims 15 and 16 were further rejected under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite with respect to various terms and phrases relating to scaled length and display features.

Response

The amendments to claim 15, from which all the other rejected claim depend, are believed to address each portion of the rejection.

In particular, claim 15 has been amended to delete the language "modules and exons," and instead recite and define "modules" as "representing a subsequence of the splice variant selected from an exon and an intron."

Claim 15 has also been amended to clarify various terms relating to scaled length and display.

Withdrawal of the rejections is respectfully requested.

V. Rejections Under 35 U.S.C. § 102

Claims 15-21 were rejected under 35 U.S.C. § 102(e) as allegedly anticipated by Loraine *et al.* (U.S. Pub. No. 2004/0049354).

The rejection is traversed in view of the foregoing amendments and following remarks.

A. The Present Claims

The present claims, as exemplified by independent claim 15, relate to "[a] method in a computer system for displaying a graphical representation of expression levels of a plurality of splice variants of a gene in one or more samples, each of the plurality of splice variants of the gene having modules, the method comprising:

identifying modules for each splice variant of the gene, each module representing a subsequence of the splice variant selected from an exon and an intron and having a length,

applying a first mathematical function to the length of a first subsequence to obtain a scaled length for the first subsequence for graphical representation,

applying a second, different, mathematical function to the length of a second subsequence to obtain a scaled length for the second subsequence for graphical representation,

determining a relative expression level for each module by applying a mathematical algorithm to expression level data obtained using exon-exon junction indicator polynucleotides that selectively hybridize to exon-exon junctions of a given splice variant, and

displaying a graphical representation wherein the modules of the given splice variants are aligned with corresponding modules or exons of other splice variants of the gene, wherein the representation indicates the relative expression levels of the modules, and wherein the scaled length of the first subsequence and the scaled length of the second subsequence are displayed simultaneously.

#### B. Summary of the Cited Art

Loraine *et al.* (U.S. Pub. No. 2004/0049354) describe computer implemented methods for analyzing splice variant data received by an input manager. The methods appear to tie known functional and experimental information to data obtained using probe sets (e.g., ¶ [0006]).

#### C. Analysis

The standard for lack of novelty, that is, for anticipation, is one of strict identity. To anticipate a claim for a patent, a single prior source must contain all its essential elements. M.P.E.P. § 2131.

The anticipation rejection over Loraine *et al.* is traversed because the cited reference does not teach all the elements of the claims, as amended. In particular, Loraine *et al.* do not teach at least the following elements of claim 15 (emphasis added):

(i) Applying a first mathematical function to the length of a first subsequence to obtain a *scaled length for the first subsequence* for graphical representation and applying a second, different, mathematical function to the length of a second subsequence to obtain a *scaled length for the second subsequence* for graphical representation;

(ii) Determining a *relative expression level* for each module by applying a mathematical algorithm to expression level data obtained using *exon-exon junction indicator polynucleotides that selectively hybridize exon-exon junctions of a given splice variant*; or

(iii) Displaying a graphical representation . . . wherein the representation indicates the *relative expression levels* of the modules, and wherein the *scaled length of*

*the first subsequence and the scaled length of the second subsequence are displayed simultaneously.*

With reference to each of the claim elements:

(i) Claim 15 requires independently scaled subsequences. Loraine *et al.* describe scaling based on base-count, *i.e.*, a single scale. (See, *e.g.*, at ¶¶ [0137], [0138], and Fig. 12.)

(ii) Claim 15 requires expression level data obtained using exon-exon junction indicator polynucleotides. Loraine *et al.* describe polynucleotides for interrogating exon-exon junctions to identify the presence of exons (*e.g.*, ¶ [0089]); however, the reference is silent as to expression data obtained using such polynucleotides.

(iii) Claim 15 requires independently-scaled subsequences displayed simultaneously. Loraine *et al.* are silent as to this feature.

Since the Loraine *et al.* do not teach at least the above elements of independent claim 15, from which the other rejected claims depend, the pending claims are not anticipated by the cited reference.

Applicants respectfully request withdrawal of the rejection.

#### VI. Conclusion

Applicants believe the foregoing amendments and remarks fully address all outstanding rejection and place the application in condition for allowance. Early notice to that effect is earnestly requested. If the Examiner has any questions or believes a telephone conference would expedite prosecution of this application, the Examiner is encouraged to call the undersigned at (650) 838-4328.

Respectfully submitted,

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